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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.71318 Seconds

(without alignments)
798.574 Million cell updates/sec

Title: US-09-622-613B-24

Sequence: 1 SNNATFOOKHIIITPICNT.....ICVKNQYVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	586.5	57.6	111	1	RNPO_RANCA
2	450	74.9	111	1	LECS_RANCA
3	369	61.4	111	1	RNPL_RANCA
4	272.5	45.3	104	1	RN30_RANPI
5	154.5	25.7	145	1	ANG3_MOUSE
6	149.5	24.9	145	1	ANGR_MOUSE
7	135.5	22.5	124	1	RNP_BALAC
8	135.5	22.5	145	1	ANGI_MOUSE
9	133.5	22.2	167	1	RNBR_BOVIN
10	132.5	22.0	124	1	RNP_PIG
11	128.5	21.4	151	1	RNBR_CARCA
12	127.5	21.2	123	1	ANG2_BOVIN
13	127.5	21.2	141	1	RNBR_GIRCA
14	127.5	21.2	151	1	RNBR_AXIPR
15	126.5	21.0	119	1	RNP_IGUIG
16	126.5	21.0	146	1	ANGI_CERAE
17	126.5	21.0	146	1	ANGI_MIOA
18	125	20.8	146	1	ANGI_SAISC
19	123.5	20.5	143	1	RNBR_SHEEP
20	122.5	20.4	124	1	RNP_SHEEP
21	122	20.3	122	1	RNP_ANTIM
22	120.5	20.0	128	1	RNP_MACRU
23	120.5	20.0	147	1	ANGI_PONPY
24	120.5	20.0	149	1	RNP_MOUSE
25	120	20.0	146	1	ANGI_MOUSE
26	119.5	19.9	123	1	ANGI_AOTTR
27	118.5	19.7	128	1	ANGI_PIG
28	118	19.6	146	1	RNBP_CAVPO
29	117.5	19.6	128	1	ANGI_SAGOE
30	116.5	19.4	124	1	RNP_HORSE
31	116.5	19.4	128	1	RNPICAMR
32	115.5	19.2	146	1	RNP_PROGU
33	114	19.0	148	1	ANGI_MACMU
					ANGI_BOVIN

34	113.5	18.9	124	1	RNP_RANCA	P00666	rangifer ta
35	113.5	18.9	125	1	ANGI_RABIT	P31347	oryctolagus
36	113.5	18.9	146	1	ANGI_PAPHA	Q8W654	papio hamad
37	113	18.8	147	1	ANGI_HUMAN	P03950	homo sapien
38	113	18.8	147	1	ANGI_PANTR	Q8W658	pan troglod
39	112.5	18.7	124	1	RNP_CARCA	P00664	capreolus c
40	112.5	18.7	124	1	RNP_GIRCA	P00662	giraffa cam
41	112.5	18.7	148	1	RML4_MOUSE	Q9JJH1	mus musculu
42	111.5	18.6	130	1	RNP_CRIO	P24717	cricetus
43	111.5	18.6	147	1	RML4_RAT	Q55004	rattus norv
44	111.5	18.6	149	1	RNP_ACOCA	Q9WU55	acomys calt
45	110.5	18.4	124	1	RNP_AEPME	P07847	aepyceos m

ALIGNMENTS

RESULT 1	ID	RNPO_RANCA	STANDARD:	PRT:	111 AA.
AC	P11916:				
DT	01-OCT-1989 (Rel. 12, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).				
OS	Rana catesbeiana (Bull. frog).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
CC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;				
OX	NCBI_TaxID=8400;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Egg;				
RX	MEDLINE=87299649; PubMed=3304421;				
RA	Titani K., Takio K., Kawada M., Nitta K., Sakakibara F., Kawachi H.,				
RA	Takayanagi G., Hakomori S.;				
RT	"Amino acid sequence of sialic acid binding lectin from frog (Rana				
RT	catesbeiana) oocytes.";				
RL	Biochemistry 26:2189-2194(1987).				
RN	[2]				
RP	CHARACTERIZATION, AND SEQUENCE OF 59-79.				
RX	MEDLINE=92220613; PubMed=1373337;				
RA	Liao Y.-D.;				
RT	"A pyrimidine-guanine sequence-specific ribonuclease from Rana				
RT	catesbeiana (bullfrog) oocytes.";				
RL	Nucleic Acids Res. 20:1371-1377(1992).				
RN	[3]				
RP	CHARACTERIZATION.				
RC	TISSUE=Egg;				
RX	MEDLINE=93192604; PubMed=8448385;				
RA	Nitta K., Oyama F., Sekiguchi K., Kawachi H.,				
RA	Takayanagi Y., Hakomori S., Titani K.;				
RT	"Ribonuclease activity of sialic acid-binding lectin from Rana				
RT	catesbeiana eggs.";				
RL	Glycobiology 3:37-45(1993).				
RN	[4]				
RP	STRUCTURE BY NMR.				
RX	MEDLINE=98437383; PubMed=9761686;				
RA	Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T. H.;				
RT	"The solution structure of a cytotoxic ribonuclease from the oocytes				
RT	of Rana catesbeiana (bullfrog).";				
RL	J. Mol. Biol. 283:231-244(1998).				
CC	- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE				
CC	RESIDUES WITH A 3'-FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)				
CC	AS SUBSTRATES, AND PREPERS THE FORMER. THE S-LECTINS IN FROG EGGS				
CC	MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG				
CC	EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING				
CC	NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND				
CC	HUMAN ORIGIN.				
CC	- SUBUNIT: MONOMER.				
CC	- SUBCELLULAR LOCATION: Secreted.				
CC	- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
CC	PIR: A27121; A27121.				

DR PDB: 1BC4: 28-OCT-98.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA: 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; 1.
 DR HydroLase: Nuclease; Endonuclease; Stalic acid; Lectin; 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 71
 FT DISULFID 34 81
 FT DISULFID 52 96
 FT DISULFID 93 110
 SO SEQUENCE 111 AA; 12464 MW; 0BC9E5F5729ECF4 CRC64;

Query Match 97.6%; Score 586.5; DB 1; Length 111;
 Best Local Similarity 99.1%; Pred. No. 1.2e-56;
 Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 NMAFPOOKHIINTPI-CNTIMDNNIYVGGCKRVNFTFISSATYKAICTGYINMNV 60
 DB 2 NMAFPOOKHIINTPIINCNITMDNNIYVGGCKRVNFTFISSATYKAICTGYINMNV 61

QY 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVGCENQYVPHFAGIGRCP 110
 DB 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVGCENQYVPHFAGIGRCP 111

RESULT 2
 LECS_RANCA STANDARD; PRT: 111 AA.
 ID LECS_RANCA
 AC P18839;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Stalic acid-binding lectin (EC 3.1.27.-).
 OS Rana japonica (Japanese reddish frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8402;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RC TISSUE=Egg;
 RX MEDLINE=9103319; PubMed=2229005;
 RA Kaniya Y., Oyama F., Sakakibara F., Nitta K., Kawachi H.,
 RT Takayanaagi Y., Tlitali K.;
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
 RT eggs.";
 RL J. Biochem. 108:139-143(1990).
 CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
 CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
 CC PREFERENTIALLY AGGLUTININATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
 CC DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: JX0120; JX0120.
 DR HSSP: P11916; 1BC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA: 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; 1.
 DR HydroLase: Nuclease; Endonuclease; Stalic acid; Lectin.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 72
 FT DISULFID 34 82
 FT DISULFID 52 97

FT DISULFID 94 111
 SQ SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 74.9%; Score 450; DB 1; Length 111;
 Best Local Similarity 78.2%; Pred. No. 6.7e-42;
 Matches 86; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

QY 2 NMAFPOOKHIINTPI-CNTIMDNNIYVGGCKRVNFTFISSATYKAICTGY-INMNV 59
 DB 2 NMAFPOOKHIINTPIINCNITMDNNIYVGGCKRVNFTFISSATYKAICTGASTNRNV 61

QY 60 LSTRFQNLNCTRTSITPRPCPYSSRTETNYICVGCENQYVPHFAGIGRCP 109
 DB 62 LSTRFQNLNCTRTSITPRPCPYSSRTETNYICVGCENQYVPHFAGIGRCP 111

RESULT 3
 RNPL_RANCA STANDARD; PRT: 111 AA.
 ID RNPL_RANCA
 AC P14626;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease, liver (EC 3.1.27.5).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=90130374; PubMed=2613682;
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
 RT Okazaki T., Ohgi K., Irie M.;
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
 RT liver.";
 RL J. Biochem. 106:729-735(1989).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: JX0085; JX0085.
 DR HSSP: P11916; 1BC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA: 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; 1.
 DR HydroLase: Nuclease; Endonuclease.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 104 104
 FT DISULFID 19 72
 FT DISULFID 34 82
 FT DISULFID 52 97
 FT DISULFID 94 111
 SO SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 61.4%; Score 369; DB 1; Length 111;
 Best Local Similarity 65.5%; Pred. No. 3.8e-33;
 Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 2 NMAFPOOKHIINTPI-CNTIMDNNIYVGGCKRVNFTFISSATYKAICTGY-INMNV 59
 DB 2 NMAFPOOKHIINTPIINCNITMDNNIYVGGCKRVNFTFISSATYKAICTGASVSPRKE 61

QY 60 LSTRFQNLNCTRTSITPRPCPYSSRTETNYICVGCENQYVPHFAGIGRCP 109
 DB 62 LSTRFQNLNCTRTSITPRPCPYSSRTETNYICVGCENQYVPHFAGIGRCP 111

ID	RN30_RANPI	STANDARD;	PRT;	104 AA.
RESULT 4				
AC	P22069.			
DT	01-AUG-1991 (Feb. 19, Created)			
DT	01-FEB-1994 (Feb. 28, Last sequence update)			
DT	01-FEB-1995 (Feb. 31, Last annotation update)			
DE	P-30 protein (EC 3.1.27.-) (oncnase).			
OS	Rana pipiens (Northern leopard frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranolidae; Rana.			
OX	NCBI_TaxID=8404;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Embryo;			
RX	MEDLINE=91093131. Pubmed=1985896;			
RA	Ardelt W., Mikulski S.M., Shogen K.;			
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens			
RT	oocytes and early embryos. Homology to pancreatic ribonucleases.";			
RL	J. Biol. Chem. 266:245-251(1991).			
RN	[2]			
RP	3D-STRUCTURE MODELING.			
RX	MEDLINE=9306155. Pubmed=1438177;			
RA	Mosimann S.C., Jones K.L., Ardelt W., Mikulski S.M., Shogen K.,			
RA	James M.N.G.;			
RT	"Comparative molecular modeling and crystallization of P-30 protein:			
RT	a novel antitumor protein of Rana pipiens oocytes and early			
RL	embryos.";			
RL	proteins 14:392-400(1992).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).			
RX	MEDLINE=94166079. Pubmed=8120892.			
RA	Mosimann S.C., Ardelt W., James M.N.G.;			
RT	"Refined 1.7 A x-ray crystallographic structure of P-30 protein, an			
RT	amphibian ribonuclease with anti-tumor activity.";			
RL	J. Mol. Biol. 236:1141-1153(1994).			
CC	-I- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY			
CC	AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR			
CC	IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH			
CC	MOLECULAR WEIGHT RIBOSOMAL RNA.			
CC	-I- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).			
CC	-I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
DR	PDB: 1ONC. 31-JAN-94.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; RNaseA; 1.			
DR	ProDom: PD000535; RNaseA; 1.			
DR	SMART: SM00092; RNase_PC; 1.			
DR	PROSITE: PS00127; RNase_PANCREATIC; 1.			
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure.			
FT	MOD_RES	1	10	10
FT	ACT_SITE	1	1	10
FT	ACT_SITE	31	31	31
FT	ACT_SITE	97	97	97
FT	DISULFID	19	68	68
FT	DISULFID	30	75	75
FT	DISULFID	48	90	90
FT	DISULFID	87	104	104
FT	HELIX	3	10	10
FT	STRAND	11	12	12
FT	HELIX	19	22	22
FT	TURN	23	24	24
FT	TURN	26	30	30
FT	STRAND	33	38	38
FT	STRAND	41	48	48
FT	HELIX	49	50	50
FT	STRAND	55	58	58
FT	STRAND	63	70	70
FT	TURN	74	75	75
FT	STRAND	77	84	84
FT	STRAND	86	91	91
FT	TURN	92	93	93
FT	STRAND	94	101	101
SEQUENCE	104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;			

Query Match	Score	DB 1:	Length	DB 2:
Best Local Similarity	45.3%	Score 272.5	DB 1: Length 104	DB 2: Length 104
Matches 54	Conservative 15	Mismatches 32	Indels 9	Gaps 4

QY	DB	Score	DB 1:	Length	DB 2:
2	WMATPOOKHINT-PIICNTFMDNNITYVGCCKRVNFIISATFYKATICTGVY-NNV 59	45.3%	Score 272.5	DB 1: Length 104	DB 2: Length 104
2	DWLIEFOKKHITNTDVEDODNIMSTNLF---HCKDKNTFIYSRPEYKALICKGILASKNV 57	45.3%	Score 272.5	DB 1: Length 104	DB 2: Length 104
60	LSTTRFQULNCTRTSITPRCPYSSKRETNICVCKENQNPVHFAGIGRC 109	45.3%	Score 272.5	DB 1: Length 104	DB 2: Length 104
58	LTTSEFYLSDC--NVTSRPCKRYKLKKSTNKEVCYENQAPVHFVGSC 104	45.3%	Score 272.5	DB 1: Length 104	DB 2: Length 104

RESULT 5	ANG3_MOUSE	STANDARD:	PRT:	145 AA.
AC	P97802:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2) (E9-5).			
GN	ANG3 OR ANGL.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OK	NCBI_TaxID=10090;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/c;			
RX	MEDLINE=97184476; PubMed=9032278;			
RA	Fu X., Kamps M.P.;			
RT	"E2a-Px1 induces aberrant expression of tissue-specific and developmentally regulated genes when expressed in NIH 3T3 fibroblasts."			
RL	Mol. Cell. Biol. 17:1503-1512(1997).			
CC	-1- FUNCTION: ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS (BY SIMILARITY)			
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
CC	-----			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC				
DR	EMBL: U72672; AAC05794.1; -			
DR	HSSP: P10152; IAGI.			
DR	MGP: MGI:1201793; Angl.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; RNaseA; 1.			
DR	PRINTS: PR00794; RIBONUCLEASE.			
DR	Prodom: PD000535; RNaseA; 1.			
DR	SMART: SM00092; RNase.Pc; 1.			
DR	PROSITE: PS00127; RNase_PANCREATIC; 1.			
KW	Hydrolase; Nuclease; Endonuclease; Angiogenesis;			
KW	Protein synthesis inhibitor; Signal.			
FT	SIGNAL	1	24	POTENTIAL.
FT	CHAIN	25	145	ANGIOGENIN-3.
FT	MOD_RES	25	25	PYROGLUTAMINE CARBOXYLIC ACID (BY SIMILARITY).
FT				
FT	ACT_SITE	37	37	BY SIMILARITY.
FT	ACT_SITE	64	64	BY SIMILARITY.
FT	ACT_SITE	137	137	BY SIMILARITY.
FT	DISULFID	50	104	BY SIMILARITY.
FT	DISULFID	63	115	BY SIMILARITY.
FT	DISULFID	81	130	BY SIMILARITY.
SO	SEQUENCE	145 AA;	16696 MW;	DE93BC92FF10682C CRC64;

DE	Angiogenin precursor (EC 3.1.27.-).
GN	ANG.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCDL_TaxID=10090.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91025023; PubMed-2222458;
RA	Bond M.D., Vallée B.L.;
RL	"Isolation and sequencing of mouse angiogenin DNA.";
RL	Biochem. Biophys. Res. Commun. 171:988-995(1990).
RP	[2]
RP	PARTIAL SEQUENCE.
RC	TISSUE-Serum;
RX	MEDLINE=93192291; PubMed-8448182;
RA	Bond M.D., Strigdom D.J., Vallée B.L.;
RT	"Characterization and sequencing of rabbit, pig and mouse
RT	angiogenins: discernment of functionally important residues and
RT	regions.";
RL	Biochim. Biophys. Acta 1162:177-186(1993).
CC	-I- FUNCTION: MAY FUNCTION AS A TNFA-SPECIFIC RIBONUCLEASE THAT BINDS
CC	TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC	ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC	PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC	FORMATION; ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC	MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC	HYDROLYZING CELLULAR RNAs.
CC	-I- SUBCELLULAR LOCATION: Secreted.
CC	-I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC	-----
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CC	or send an email to license@sib-sib.ch).
CC	-----
DR	EMBL; U22516; AAA91366.1; .
DR	PIR; A35932; A35932.
DR	HSSP; P03950; 1A4Y.
DR	MGI; MGI:88022; Ang.
DR	InterPro: IPR001437; RNaseA.
DR	Pfam: PF00074; rnaaseA.1.
DR	PRINTS: PR00794; RIBONUCLEASE.
DR	ProDom: PD000535; RNaseA.1.
DR	SMART: SM00042; RNase_Pc.1.
DR	PROSITE: PS00127; RNASE_PANCREATIC.1.
KM	Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KV	protein synthesis inhibitor; signal.
FT	SIGNAL 1 24
FT	CHAIN 25 145
FT	MOD_RES 25 25
FT	-----
FT	ANGIOENIN.
FT	PYROLIDONE CARBOXYLIC ACID (BY
FT	SIMILARITY).
FT	BY SIMILARITY.
FT	ACT_SITE 37 37
FT	ACT_SITE 64 64
FT	ACT_SITE 137 137
FT	DISULFD 50 104
FT	DISULFD 63 115
FT	DISULFD 81 130
FT	BY SIMILARITY.
SO	SEQUENCE 115 AA; 16228 MW; 069444260BB764938 CRC64;
Oy	Query Match 22.5%; Score 135.5; DB 1; Length 145;
Oy	Best Local Similarity 39.5%; Pred. No. 8, 1e-08;
Oy	Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3
Dy	33 CRKVTFTLISSATYTKAIC--TGVIINNV-LSTRFQNLCTRTSTIPR-PCPYSSRTE 87
Dy	: : : :
Dy	63 CKCVMTFLHGKSNIKAIKGANGSPYREURLRMSSKSPFOYTTCKHGGSGPPRCQYRASAG 122
Oy	88 THVICVCENQCPVHF 103
Oy	: :

RESULT 9	STANDARD:	PRT:	167 AA.
NRBR_BOVIN			
AC P39873;			
DT 01-FEB-1995 (Rel. 31, Created)			
DT 01-FEB-1995 (Rel. 31, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE Ribonuclease, brain precursor (EC 3.1.27.-) (BRB) ..			
CN BRN.			
OC Bos taurus (Bovine).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC Bovidae; Bovinae; Bos.			
OX NCBI_TaxID=9913;			
RP [1]			
RP SEQUENCE FROM N.A.			
RA MEDLINE=92093604; Pubmed=1754384;			
RA Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,			
RA Viola M., Palmieri M., Russo E., Furia A.;			
RA "Molecular cloning of the gene encoding the bovine brain ribonuclease			
RT and its expression in different regions of the brain.";			
RL Nucleic Acids Res. 19:6469-6474(1991).			
[2]			
RP SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.			
RC TISSUE=Brain;			
RX MEDLINE=89214015; Pubmed=3243767;			
RA Watanabe H., Katoh H., Ishii M., Komoda Y., Sando A., Takizawa Y.,			
RA Ohgi K., Irie M.;			
RA "Primary structure of a ribonuclease from bovine brain."			
RL J. Biochem. 104:939-945(1988).			
[3]			
RP SEQUENCE OF 27-167 FROM N.A.			
RA MEDLINE=96139017; Pubmed=8587129;			
RA Confalone E., Belmonte J.J., Sasso M.P., Carsana A., Palmieri M.,			
RA Vento M.T., Furia A.;			
RT "Molecular evolution of genes encoding ribonucleases in ruminant			
RT species.";			
RL J. Mol. Evol. 41:850-858(1995).			
[4]			
CC - SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
CC -----			
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CC or send an email to license@sib-sib.ch).			
CC -----			
DR EMBL: X59767; CAA42439.1; -			
DR EMBL: S81744; AAB36138.1; -			
DR PIR: S20066; S20066.			
DR PIR: JX0056; JX0056.			
DR HSSP: P00656; 2RMS.			
DR GLYCOSITEDB: P39873; -			
DR InterPro: IPR001427; RNaseA.			
DR Pfam: PF00074; RNaseA; 1.			
DR PRINTS: PR00794; RIBONUCLEASE.			
DR ProDom: PD000535; RNaseA; 1.			
DR SMART: SM00092; RNase_Pc; 1.			
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.			
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.			
FT SIGNAL	1	26	
FT CHAIN	27	167	RIBONUCLEASE, BRAIN.
FT ACT_SITE	38	38	BY SIMILARITY.
FT ACT_SITE	67	67	BY SIMILARITY.
FT ACT_SITE	145	145	BY SIMILARITY.
FT DISULFID	52	110	BY SIMILARITY.
FT DISULFID	66	121	BY SIMILARITY.
FT DISULFID	84	136	BY SIMILARITY.
FT DISULFID	91	98	BY SIMILARITY.

FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 155 155 /FTID=CAR_000005.
 FT CARBOHYD 159 159 O-LINKED.
 FT CONFLICT 155 155 T -> S (IN REF. 2).
 SQ SEQUENCE 167 AA: 18450 MW: 6181ACAC3CC2FC459 CRC64;

Query Match
 Best Local Similarity 31.4%; Pred. No. 1.5e-07;
 Matches 38: Conservative 17; Mismatches 43; Indels 23; Gaps 7;

OY 4 ATPQKH-----INPILICNTIMNNIYIVGGCKRVNFISSATTVAICGVINM 57
 Db 32 AKFRQHDSSSSSSNNYCNQMKRR-RMTHGRCKPVNTFVHESLDDVAVCS---QK 87
 OY 58 NVL-----STRQLNTCTRTSTPRP-CYSSRTETNYICVKE-NOY-PVHEA 104
 Db 88 NITCKNGHPNCOYQSKSTWSTIDCRETGSSKYPNCAYKTSQKXITVACEGNPYPVHEF 147
 OY 105 G 105
 Db 148 G 148

RESULT 10

RNP_PIG ID RNP_PIG STANDARD: PRT: 124 AA.
 AC P00671:
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 GN RNASE1 OR RN51.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=70104197; PubMed=5460946;
 RA Jackson R.L., Hirs C.H.W.;
 RT "The primary structure of porcine pancreatic ribonuclease. II. The
 RT amino acid sequence of the reduced S-aminoethylated protein.";
 RL J. Biol. Chem. 245:637-653(1970).
 RN [2]
 RP REVISION TO 2.
 RA Mierenga R.K., Huizinga J.D., Gaastra W., Wellings G.W., Beintema J.J.;
 RT "Affinity chromatography of porcine pancreatic ribonuclease and
 RT reinvestigation of the N-terminal amino acid sequence.";
 RL FEBS Lett. 31:181-185(1973).
 RN [3]
 RP DISULFIDE BONDS.
 RX MEDLINE=70104198; PubMed=4904878;
 RA Phelan J.J., Hirs C.H.W.;
 RT "The primary structure of porcine pancreatic ribonuclease. 3. The
 RT disulfide bonds.";
 RL J. Biol. Chem. 245:654-661(1970).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00816; NREG.
 DR HSSP: P00656; ISRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR PRODOM: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW CARBOHYD
 FT Hydroxide Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84

FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT ACT_SITE 12 12
 FT ACT_SITE 41 41
 FT ACT_SITE 119 119
 FT CARBOHYD 21 21
 FT CARBOHYD 34 34
 FT CARBOHYD 76 76
 SQ SEQUENCE 124 AA: 13804 MW: 0AC28CDE14111845 CRC64;

Query Match
 Best Local Similarity 31.6%; Pred. No. 1.4e-07;
 Matches 36: Conservative 19; Mismatches 42; Indels 17; Gaps 6;

OY 6 FOQKH-----INPILICNTIMNNIYIVGGCKRVNFISSATTVAICGVINM 57
 Db 8 FORQHDSSSSSSNNYCNLMGRR-NMTHGRCKPVNTFVHESLDDVAVCSQINVC 66
 OY 59 VLSTRQLNT-----CTRTSTPRP-CYSSRTETNYICVKE-NOY-PVHEF 103
 Db 67 NGOTCYQSNSTHMTIDCRGTGSSKYPNCAYKASQEQKHITVACEGNPYPVHEF 120

RESULT 11

RNB_CAPCA ID RNB_CAPCA STANDARD: PRT: 151 AA.
 AC P79351:
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
 OS Capreolus capreolus (Roe deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
 OC Cervidae; Odocoileinae; Capreolus.
 OX NCBI_TaxID=9858;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98278842; PubMed=9611269;
 RA Breukelman H.J., Van der Munnik N., Kleineldam R.G., Furia A.,
 RA Beintema J.J.;
 RT "Secretory ribonuclease genes and pseudogenes in true ruminants.";
 RL Gene 212:259-268(1998).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: Y11673; CA72371.1; -
 DR HSSP: P00656; ISRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR PRODOM: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydroxide Nuclease; Endonuclease; Glycoprotein.
 FT ACT_SITE 41 41
 FT DISULFID 26 84
 FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT CARBOHYD 62 62
 FT CARBOHYD 129 129
 FT CARBOHYD 133 133
 SQ SEQUENCE 151 AA: 16971 MW: 392D0E6302F006A6 CRC64;

Query Match 21.4% Score 128.5; DB 1; Length 151;
 Best Local Similarity 29.4%; Pred. No. 4.8e-07;
 Matches 35; Conservative 17; Mismatches 44; Indels 23; Gaps 6;

OY 4 ATPCKHII-----INPIICNTIMDNNIIVGGCKRVNFTIISATVKAICTGYINM 57
 DB 6 AKFRHMDSSSSSSGNNPCNOMMKRR-RMTGRCRCPVNFVHESLDNVAVCS---QK 61
 OY 58 NVL-----STTRQLNCTRTSITPPR-CPYSSRTENIYCVKCEMG--YVPHF 103
 DB 62 NITCKNCPNCYQSNSTNMTIDCKRTGSSSKTPNCATKTSOKOKYITVACEDDPYVPHF 120

RESULT 12

ANG2_BOVIN STANDARD: PRT: 123 AA.

AC P80929; 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiogenin-2 (EC 3.1.27.-).

OS Bos taurus (Bovine);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;

SEQUENCE.

RC TISSUE-Serum, and Milk;
 RX MEDLINE=97409980; PubMed=9266695;

RA Strydom D.J., Bond M.D., Vallée B.L.;

RT "An angiogenic protein from bovine serum and milk -- purification and
 primary structure of angiogenin-2";

RL Eur. J. Biochem. 247:535-544(1997);

CC -1- FUNCTION: BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND
 HAS VERY LOW RIBONUCLEASE ACTIVITY. HAS POTENT ANGIOGENIC
 CC ACTIVITY. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAS.

CC -1- TISSUE SPECIFICITY: SERUM, AND MILK.

CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

DR HSSP; P10152; IAGI.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR PRINTS: PR00794; RIBONUCLEASE.

DR PRODOM: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase_Pc; 1.

DR PROSITE: PS00127; RNASE_PANCREATIC; 1.

KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
 Protein synthesis inhibitor; Glycoprotein.

FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.

FT ACT_SITE 12 12 BY SIMILARITY.

FT ACT_SITE 39 39 BY SIMILARITY.

FT ACT_SITE 113 113 BY SIMILARITY.

FT DISULFID 25 80 BY SIMILARITY.

FT DISULFID 38 91 BY SIMILARITY.

FT DISULFID 56 106 BY SIMILARITY.

FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .).

SO SEQUENCE 123 AA; 14522 MW; B703B983919FD2P CRC64;

Query Match 21.2% Score 127.5; DB 1; Length 123;
 Best Local Similarity 30.6%; Pred. No. 5e-07;
 Matches 33; Conservative 19; Mismatches 43; Indels 13; Gaps 5;

OY 6 FOQKHIIPT-----ICNTIMDNNIIVGGCKRVNFTIISATVKAICTGYINM 57
 DB 8 FLRRHYDSEFTGHDRYCTFMERR--NMTPRCKDTNFTIGNSDDIAYVDDRNGEPR 65

OY 58 NVLSTIR--FOLNCTRTSITPPR-CPYSSRTENIYCVKCEMG--YVPHF 102
 DB 66 NGLRRSPFOVYTCRRHGSPRPRCRYRAFRANRVIYICRGDGPPI 113

RESULT 13

RNRB_GIRCA STANDARD: PRT: 141 AA.

AC Q29542; Q29533;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).

OS Giraffa camelopardalis (Giraffe).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffidae;
 OC Giraffidae; Giraffa.

NCBI_TaxID=9894;

SEQUENCE FROM N.A.

RP MEDLINE=96139017; PubMed=8587129;

RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmeri M.,

RA Vento M.T., Furia A.;

RT "Molecular evolution of genes encoding ribonucleases in ruminant

RT species";

RL J. Mol. Evol. 41:850-858(1995).

SEQUENCE OF 31-114 FROM N.A.

RP MEDLINE=93367815; PubMed=8360916;

RA Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,

RA Carsana A., Palmeri M., Furia A.;

RT "Sequences related to the ox pancreatic ribonuclease coding region in

RT the genomic DNA of mammalian species";

RL J. Mol. Evol. 37:29-35(1993).

CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

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DR EMBL; S81743; AAB36137.1; -

DR EMBL; S65126; AAB27931.1; -

DR HSSP; P00656; 2RNS.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR PRINTS: PR00794; RIBONUCLEASE.

DR PRODOM: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase_Pc; 1.

DR PROSITE: PS00127; RNASE_PANCREATIC; 1.

KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.

FT ACT_SITE 41 41 BY SIMILARITY.

FT DISULFID 26 84 BY SIMILARITY.

FT DISULFID 40 95 BY SIMILARITY.

FT DISULFID 58 110 BY SIMILARITY.

FT DISULFID 65 72 BY SIMILARITY.

FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (BY SIMILARITY).

FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).

SO SEQUENCE 141 AA; 15592 MW; 73745FE9079591F CRC64;

Query Match 21.2% Score 127.5; DB 1; Length 141;
 Best Local Similarity 30.6%; Pred. No. 5.7e-07;
 Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

OY 4 ATPCKHII-----INPIICNTIMDNNIIVGGCKRVNFTIISATVKAICTGYINM 57
 DB 6 AKFRHMDSSSSSSGNNPCNOMMKRR-RMTGRCRCPVNFVHESLDNVAVCS---QK 61

OY 58 NVL-----STTRQLNCTRTSITPPR-CPYSSRTENIYCVKCEMG--YVPHF 104
 DB 62 NITCKNCPNCYQSNSTNMTIDCKRTGSSSKTPNCATKTSOKOKYITVACEDDPYVPHF 121

OY 105 G 105

```

DB      122 G 122

RESULT 14
RNRB_AXIPR      STANDARD:      PRT:      151 AA.
ID      RNRB_AXIPR
AC      P87350:
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN      Brn.
OS      Axis porcinus (Hog deer).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC      Cervidae; Cervinae; Axis.
OX      NCBI_Taxid=57737;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98278842; PubMed=9611269;
RA      Breukelman H.J., van der Munnik N., Kleineldam R.G., Furia A.,
RA      Beintema J.J.;
RT      "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL      Gene 212:259-268(1998).
CC      -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: Y11670; CAI72368.1;
DR      HSSP: P00656; 1SRN.
DR      InterPro: IPR001427; RNaseA.
DR      Pfam: PF00074; RNaseA.
DR      PRINTS: PR00794; RIBONUCLEASE.
DR      ProDom: PD000535; RNaseA.
DR      SMART: SM00092; RNase_Pc.
DR      PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW      Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT      ACT_SITE 41
FT      DISULFID 26
FT      DISULFID 40
FT      DISULFID 58
FT      DISULFID 65
FT      CARBOHYD 62
FT      CARBOHYD 129
FT      CARBOHYD 133
SQ      SEQUENCE 151 AA; 16819 MW; E95F3757EFC5B233 CRC64;

Query Match      21.2%; Score 127.5; DB 1: Length 151;
Best Local Similarity 30.8%; Pred. No. 6.2e-07;
Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

OY      4      ATFOOKHI-----INPIICNTIMDNIIYVGGCKRVNFTIISATTVAICGVLM 57
DB      6      AKFRROHMDAGSSSSGNSNYCNQMKRR-RMTHGCKRVNFTVHESLDSVKAACS--QK 61
OY      58      NVL-----STTRFOLNTCTRTSITPRP-CPYSSRTETNYICVKE-NQY-PVHFA 104
DB      62      NITCKNGOPNCYQNSFTWNTIDCRETGSSKYPNCAYKTSQKOKYITVACEGNPVPHFD 121
OY      105      G 105
DB      122      G 122

```

RESULT 15
RNP_IGUG

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ID      RNP_IGUG      STANDARD:      PRT:      119 AA.
AC      P80287;
DT      01-FEB-1994 (Rel. 28, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Iguana iguana (Common Iguana).
OS      Iguana iguana (Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX      NCBI_Taxid=8517;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Pancreas;
RX      MEDLINE=94139745; PubMed=8307028;
RA      Zhao W., Beintema J.J., Hofsteenge J.;
RT      "The amino acid sequence of iguana (Iguana iguana) pancreatic
RT      ribonuclease.";
RL      Eur. J. Biochem. 219:641-646(1994).
CC      -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC      phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC      with 2',3'-cyclic phosphate intermediates.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- TISSUE SPECIFICITY: PANCREAS.
CC      -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR      HSSP: P00656; 1LSO.
DR      InterPro: IPR001427; RNaseA.
DR      Pfam: PF00074; RNaseA.
DR      PRINTS: PR00794; RIBONUCLEASE.
DR      ProDom: PD000535; RNaseA.
DR      SMART: SM00092; RNase_Pc.
DR      PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW      Hydrolyase; Nuclease; Endonuclease.
FT      MOD_RES 1
FT      DISULFID 25
FT      DISULFID 39
FT      DISULFID 57
FT      ACT_SITE 10
FT      ACT_SITE 40
FT      ACT_SITE 113
SQ      SEQUENCE 119 AA; 13324 MW; 6072FB5B7B15BD5A CRC64;

Query Match      21.0%; Score 126.5; DB 1: Length 119;
Best Local Similarity 29.8%; Pred. No. 6.2e-07;
Matches 34; Conservative 16; Mismatches 51; Indels 13; Gaps 4;

OY      2      NMATFOOKHI-----INPIICNTIMDNIIYVGGCKRVNFTIISATTVAIC--- 51
DB      2      DWSSFOQKHIDYPTTSASNPAYCDLMMQRR-NLNPYCKTRNFTVHASPSEIDQVCGSG 60
OY      52      TGVINMNVLSSTTRFOLNTCTRTSIT-PRCPYSSRTETNYICVKEHQYVPHF 103
DB      61      GTHEDNLVDYDNESFDLIDCKNVGTVAPSSCKYNGTPTKRIACENQPVPHF 114

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Search completed: June 25, 2003, 14:50:07
Job time : 5.71318 secs